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BIOTECHNOLOGY
SYSTEMS
BRANCH

6 2001

ER 1600/2900

RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/757,333A

Source: 16/9

Date Processed by STIC: 5/30/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
- 2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO).

Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/757,333A

DATE: 05/30/2001
TIME: 11:47:47

Input Set : A:\PTO.txt
Output Set: C:\CRF3\05302001\I757333A.raw

2 <110> APPLICANT: Achilefu, Samuel I.
 3 Rajagopalan, Raghavan
 4 Dorshow, Richard B.
 5 Bugaj, Joseph E.
 7 Mallinckrodt Inc.
 9 <120> TITLE OF INVENTION: Versatile Hydrophilic Dyes
 11 <130> FILE REFERENCE: MRD-67
 13 <140> CURRENT APPLICATION NUMBER: US 09/757,333A
 14 <141> CURRENT FILING DATE: 2001-01-09
 16 <150> PRIOR APPLICATION NUMBER: US 09/484,321
 17 <151> PRIOR FILING DATE: 2000-01-18
 19 <160> NUMBER OF SEQ ID NOS: 8
 21 <170> SOFTWARE: FastSEQ for Windows Version 3.0
 23 <210> SEQ ID NO: 1
 24 <211> LENGTH: 8
 25 <212> TYPE: PRT
 26 <213> ORGANISM: Artificial Sequence
 28 <220> FEATURE:
 W--> 29 <221> NAME/KEY: MOD RES *OK*
 30 <222> LOCATION: (1)...(7)
 31 <223> OTHER INFORMATION: Xaa at location 1 represents D-Phe.
 32 <223> OTHER INFORMATION: Xaa at locations 2 and 7 represents Cys with an
 33 intramolecular disulfide bond between two Cys
 34 amino acids.
 35 <223> OTHER INFORMATION: Xaa at location 4 represents D-Trp.
 37 <400> SEQUENCE: 1
WOK 38 Xaa Xaa Tyr Xaa Lys Thr Xaa Thr
 39 1 5
 42 <210> SEQ ID NO: 2
 43 <211> LENGTH: 8
 44 <212> TYPE: PRT
 45 <213> ORGANISM: Artificial Sequence
 47 <220> FEATURE: *same end*
 W--> 48 <221> NAME/KEY: MOD RES
 49 <222> LOCATION: (1)...(8)
 50 <223> OTHER INFORMATION: Xaa at location 1 represents D-Phe.
 51 <223> OTHER INFORMATION: Xaa at locations 2 and 7 represents Cys with an
 52 intramolecular disulfide bond between two Cys
 53 amino acids.
 54 <223> OTHER INFORMATION: Xaa at location 4 represents D-Trp.
 55 <223> OTHER INFORMATION: Xaa at location 8 represents Thr-OH.
 57 <400> SEQUENCE: 2
WOK 58 Xaa Xaa Tyr Xaa Lys Thr Xaa Xaa
 59 1 5
 61 <210> SEQ ID NO: 3
 62 <211> LENGTH: 11
 63 <212> TYPE: PRT

Does Not Comply
Corrected Diskette Needed

pp 1-3

see item 11 on Err Summary Sheet

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/757,333A

DATE: 05/30/2001
TIME: 11:47:47

Input Set : A:\PTO.txt
Output Set: C:\CRF3\05302001\I757333A.raw

64 <213> ORGANISM: Artificial Sequence *same*
 66 <220> FEATURE:
 W--> 67 <221> NAME/KEY: MOD RES
 68 <222> LOCATION: (1)...(0)
 W--> 70 <223> OTHER INFORMATION:
 70 <400> SEQUENCE: 3
 71 Gly Ser Gly Gln Trp Ala Val Gly His Leu Met
 72 1 5 10
 75 <210> SEQ ID NO: 4
 76 <211> LENGTH: 11
 77 <212> TYPE: PRT
 78 <213> ORGANISM: Artificial Sequence
 80 <220> FEATURE:
 81 <221> NAME/KEY: MOD_RES
 82 <222> LOCATION: (1)...(0)
 W--> 84 <223> OTHER INFORMATION:
 84 <400> SEQUENCE: 4
 85 Gly Asp Gly Gln Trp Ala Val Gly His Leu Met
 86 1 5 10
 89 <210> SEQ ID NO: 5
 90 <211> LENGTH: 8
 91 <212> TYPE: PRT
 92 <213> ORGANISM: Artificial Sequence
 94 <220> FEATURE:
 95 <221> NAME/KEY: MOD_RES
 96 <222> LOCATION: (1)...(0)
 W--> 98 <223> OTHER INFORMATION:
 98 <400> SEQUENCE: 5
 99 Asp Tyr Met Gly Trp Met Asp Phe
 100 1 5
 103 <210> SEQ ID NO: 6
 104 <211> LENGTH: 8
 105 <212> TYPE: PRT
 106 <213> ORGANISM: Artificial Sequence
 108 <220> FEATURE:
 W--> 109 <221> NAME/KEY: MOD RES
 110 <222> LOCATION: (1)...(6)
 111 <223> OTHER INFORMATION: Xaa at locations 3 and 6 represents Norleucine.
 113 <400> SEQUENCE: 6
OK 114 Asp Tyr Xaa Gly Trp Xaa Asp Phe
 115 1 5
 117 <210> SEQ ID NO: 7
 118 <211> LENGTH: 8
 119 <212> TYPE: PRT
 120 <213> ORGANISM: Artificial Sequence
 122 <220> FEATURE:
 W--> 123 <221> NAME/KEY: MOD RES
 124 <222> LOCATION: (1)...(6)
 125 <223> OTHER INFORMATION: Xaa at location 1 represents D-Asp.

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/757,333A

DATE: 05/30/2001
TIME: 11:47:47

Input Set : A:\PTO.txt
Output Set: C:\CRF3\05302001\I757333A.raw

126 <223> OTHER INFORMATION: Xaa at locations 3 and 6 represents Norleucine.

128 <400> SEQUENCE: 7

W--> 129 Xaa Tyr Xaa Gly Trp Xaa Asp Phe

130 1 5

133 <210> SEQ ID NO: 8

134 <211> LENGTH: 8

135 <212> TYPE: PRT

136 <213> ORGANISM Artificial Sequence

138 <220> FEATURE:

W--> 139 <221> NAME/KEY: MOD RES

140 <222> LOCATION: (1)...(1)

141 <223> OTHER INFORMATION: Xaa at location 1 represents D-Lys.

143 <400> SEQUENCE: 8

W--> 144 Xaa Pro Arg Arg Pro Tyr Ile Leu

145 1 5

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/757,333A

DATE: 05/30/2001

TIME: 11:47:48

Input Set : A:\PTO.txt

Output Set: C:\CRF3\05302001\I757333A.raw

L:29 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:1
L:38 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:48 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:2
L:58 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:67 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:3
L:70 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:84 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:98 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:109 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:6
L:114 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:123 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:7
L:129 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:139 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:8
L:144 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER: 09/757,333A

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleic
 Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 Misaligned Amino
 Numbering The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 Variable Length Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 PatentIn 2.0
 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 Skipped Sequences
(OLD RULES) Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
 (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 Skipped Sequences
(NEW RULES) Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000
- 9 Use of n's or Xaa's
(NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10 Invalid <213>
Response Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11 Use of <220>
J Sequence(s) 1-8 missing the <220> "Feature" and associated numeric identifiers and responses.
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 PatentIn 2.0
 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.